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(54) Title: COMPOSITIONS AND METHODS FOR GENE SILENCING

(57) Abstract: DNA constructs are provided for disrupting gene expression in targeted organisms.



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Compositions and Methods for Gene Silencing**By Monica Driscoll****Nektarios Tavernarakis****5 FIELD OF THE INVENTION**

This invention relates the fields of molecular biology and gene silencing. More specifically, the invention provides compositions and methods for heritable and inducible gene silencing in target organisms.

10 BACKGROUND OF THE INVENTION

Several publications are referenced in this application in order to more fully describe the state of the art to which this invention pertains. Complete citations may be found at the end of the specification. The disclosure of each of these publications is incorporated by reference herein.

RNA interference was discovered by Guo and Kemhues in the course of attempts to use antisense RNA to block gene expression in the maternal germ line. To their surprise, they found that both antisense and sense RNA preparations induced remarkably precise phenocopies of the targeted gene. Since then, both the efficacy and apparent lack of strand specificity associated with this interference process have been borne out in many subsequent studies. The mystery surrounding the mechanism of interference was recently deepened with the discovery that double-stranded RNA (dsRNA) is at least an order of magnitude more potent at inducing interferences than are preparations of either single strand. The surprising properties of this interference mechanism prompted users to abandon the term "antisense" and to begin referring to the process merely as "RNA interference". The robust nature of the interference

effect and the high degree of specificity have allowed RNAi to gain wide acceptance as a reverse genetic tool.

To date, most of these studies entail the microinjection of dsRNA duplexes corresponding to particular segments of targeted genes. While these methods are effective most of the time, the phenotype is not inherited. Accordingly, subsequent generations of targeted organisms must be continuously microinjected in order to attain the desired gene silencing effects. Likewise the technique is limited to organisms which are amenable to injection or application of dsRNA. It is an object of the present invention to overcome these limitations of the prior art.

SUMMARY OF THE INVENTION

The present invention is directed to materials and methods which facilitate gene silencing in targeted organisms. In one embodiment of the invention, a DNA construct encoding an inverted repeat gene is provided. The construct comprises i) a promoter element operably linked in a 5' to 3' direction to a first coding sequence and a second sequence, the first coding sequence being in a sense orientation, the second sequence being the first coding sequence in an antisense orientation linked to the 3' end of the first coding sequence; and ii) a transcription termination element operably linked 3' to said first and second coding sequences. In an alternative embodiment, the first coding sequence of the IR construct is in an antisense orientation and the second coding sequence is in a sense orientation. In a preferred aspect of the invention, the inverted repeat gene of the invention is inserted into an expression vector.

In a preferred embodiment, the DNA constructs of the invention contain an inducible promoter to maximize

expression of the inverted repeat genes of the invention. It should be apparent to those of skill in the art however that any promoter which acts to drive expression of the inverted repeat genes are also within the scope of the invention. Promoters contemplated for use in the DNA construct described above include, without limitation, heat shock promoters, metallothioneine promoter, glucocorticoid promoter, CMV promoter, SV40 promoter, nervous system specific C. elegans promoters, such as unc-119, mec-4, odr-4, and muscle promoters such as unc-54, myo-2, act-1 and ben-1. Optionally, the DNA constructs of the invention may include a spacer sequence between the first coding and second sequences. Such spacer sequences can be about 300, 500, 700, 1000 or 1500 nucleotides in length.

In yet another aspect of the invention, host cells containing the DNA constructs encoding the inverted repeat genes of the invention are provided. Such cells include, by way of illustration, C. elegans, yeast, Dictostelium, drosophila, mice, plants, insects, human cells and other nematodes

Methods for production of phenocopy knock out mutants via introduction of an inverted repeat gene into a target organism are also provided. The inverted repeat genes of the invention may be introduced into target organisms, such as C. elegans, via a process selected from the group consisting of microinjection, soaking, and DNA coated particle bombardment. Suitable targets for gene silencing include the following: green fluorescent protein gene, C3782.5, F26F12.7, T14G8.1, efk-1, mec-4, unc-8, unc-119, degenerinis ZB770.1, T28B8.5, T28F24.2, C24G7.2 and T28D9.7.

Several exemplary IR gene construct expression vectors are provided herein. IR gene constructs for reducing or inhibiting the expression of the beta

amyloid protein are shown in Figure 4. IR gene
construct expression vectors for inhibiting or reducing
the expression of alpha-synuclein are provided in Figure
5. An exemplary vector for inhibiting geminivirus
infection in tomato is provided in Figure 6.

According to one aspect of the present invention, a
method is provided for inhibiting or preventing the
production of a pre-determined protein in a living
organism. The method comprises providing a vector
encoding IR ds RNA molecules which are capable of
binding specifically to an mRNA sequence of interest.
The vectors encoding the IR gene constructs of the
invention are administered to the living organism under
conditions whereby the vector enters cells, is expressed
and thereafter specifically binds to the nucleic acid
encoding the protein of interest, in an amount
sufficient to reduce or inhibit production of the
protein of interest.

According to another aspect of the present
invention, a method is provided for treating a
pathological condition related to an abnormal
accumulation of disease-associated proteins. Examples
of such abnormal pathological conditions include,
without limitation, Alzheimer's disease, Parkinson's
and Huntington's Disease. The method comprises
administering to a patient having such a pathological
condition a pharmaceutical preparation comprising vector
having an IR gene construct contained therein capable of
entering a cell expressing the protein of interest.
Expression of the IR gene construct results in the
generation of a nucleic acid molecule which specifically
binds to a nucleic acid encoding the protein of
interest, in an amount sufficient to affect the level of
production of the protein of interest, thereby
alleviating the pathological condition.

According to another aspect of this invention, a pharmaceutical preparation is provided for treating a pathological condition related to the abnormal accumulation of disease-related proteins. This pharmaceutical preparation comprises, in a biologically compatible medium, a vector having an IR gene construct contained therein capable of entering a cell and causing targeted gene silencing, in an amount sufficient to inhibit or reduce the level of production of the disease-associated protein. The biologically compatible medium is preferably formulated to enhance the lipophilicity and membrane-permeability of the IR gene construct expression vector.

The use of an inverted repeat RNAi expression construct as a delivery vehicle exploits the ability of such a vector to continue to generate multiple dsRNA copies, thereby prolonging the expression of the inhibitory RNA molecules indefinitely *in vivo*. This feature presents a distinct advantage over that of conventional modes for introduction of dsRNA, which provide a nonrenewable source of dsRNA in a one time delivery system. The methods and IR RNAi expression vectors of the present invention provide notable advantages over currently available compounds and methods for treating diseases associated with the abnormal expression, or accumulation of proteins in cells observed in many viral and neurodegenerative disorders.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides a schematic drawing of an IR gene construct expression vector of the invention.

Figures 2A and 2B depict the strategy for

generation of heritable and inducible RNAi in the nematode. A strong inducible promoter is fused to a direct inverted repeat gene. Upon induction of expression in transgenic animals harboring this gene, transcripts are generated which fold back in a uni-molecular reaction to generate double stranded RNA within all cells that express the heat shock gene. The size of the single stranded loop that occurs after foldback is not known (Fig. 2A). Construction of inducible inverted repeat genes is shown in Fig. 2B. Exon-rich genomic DNA (or cDNA) is amplified using two primers that introduce unique restriction sites at the fragment ends. One restriction site is used to generate the inverted repeat and is ultimately situated at the inversion point (IP). The other restriction site (designated as end) is ultimately used to join the inverted repeat to the vector. Amplified fragments are digested with the enzyme situated at the IP restriction site (IPRS) and ligated together. Digestion at the end restriction site (ERS) enables the fragment to be cloned into a similarly digested, CIAP-treated *C. elegans* expression vector. In our work, vector pPD49.78²², which includes the *hsp16-2* promoter and the 3' untranslated region of muscle myosin *unc-54*, was utilized (Fig. 2B).

Figures 3A and 3B show that double stranded RNA synthesized *in vivo* can disrupt *C. elegans* gene expression. Fig. 3A: Enzymatic assay for *in vivo* RNAi-induced disruption of the eEf2 kinase gene. CeEFK-1 activity was assayed as described¹¹ in reactions in which 0.5µg rabbit reticulocyte eEF-2 was added to worm protein extracts. Arrow indicates the eEF-2 protein position. Lane 1, Wild type ; lane 2, line harboring extrachromosomal *hsp16-2_pCefk-1(IR)*, non-heat shocked; lane 3, a transgenic line harboring extrachromosomal

parental vector pPD49.78, heat shocked; lane 4, line harboring extrachromosomal *hsp16-2_pCefk-1(IR)*, heat shocked; lane 5, Tc1 insertion *Cefk-1* mutant. Fig. 3B: Use of *in vivo* RNAi to disrupt GFP expression in neurons and pharyngeal muscle. Progeny of transgenic lines harboring extrachromosomal *unc-119_pGFP* (panels 1, 4; *unc-119* is expressed in all neurons¹³), integrated *mec-4_pGFP* (panels 2,5; *mec-4* is expressed in six touch sensory neurons¹⁴) or *myo-2_pGFP* (panels 3, 6; *myo-2* is expressed in pharyngeal muscle¹⁶) and *hsp16-2_pGFP(IR)* were compared at 20 °C or consequent to parental heat shock at the L4 stage (35 °C, 4 h). Progeny of similarly heat-shocked *unc119_pGFP*, *mec-4_pGFP* or *myo-2_pGFP* lines exhibited no apparent reduction in intensity of neuronal fluorescence (data not shown). In parallel conventional RNAi experiments, 6 of 210 progeny of an *unc-119_pGFP* parent, 11 of 270 progeny of a *mec-4_pGFP* parent, and 57 of 240 progeny of a *myo-2_pGFP* parent exhibited detectable reduction in GFP signal.

Figure 4 is a schematic diagram of an IR gene construct expression vector suitable for inhibiting or reducing expression of the beta-amyloid protein.

Figure 5 is a schematic diagram of an IR gene construct expression vector suitable for inhibiting or reducing expression of the α -synuclein protein.

Figure 6 is an schematic diagram of an IR gene construct expression vector suitable for expressing the NP protein of a tomato geminivirus thereby inhibiting viral replication in the targeted tomato plant.

The detailed description set forth below describes preferred methods for practicing the present invention. Methods for selecting and preparing the IR gene constructs of the invention and expression vectors containing the same are described, as well as methods for administering the IR gene construct containing compositions *in vivo*. Specific *in vitro* and *in vivo* diagnostic and therapeutic applications of the IR gene construct compositions are also set forth.

DETAILED DESCRIPTION OF THE INVENTION

Double-stranded RNA interference (RNAi) is an effective method for disrupting specific gene expression in *C. elegans* and other organisms¹⁻⁵. However, this powerful reverse genetics tool is most often employed in nematodes and plants because introduced dsRNA is not stably inherited¹. Another difficulty is that late-acting genes are not as efficiently knocked-out by RNAi as embryonically expressed genes. This may be due to a lowering of the concentration of dsRNA as cellular division proceeds during organismal development¹. In particular, some neuronally expressed genes appear refractory to dsRNA-mediated interference. It is an object of the invention to extend the applicability of RNAi by the controlled *in vivo* expression of heritable inverted-repeat (IR) genes. The efficacy of *in vivo*-driven RNAi has been assessed in three situations for which heritable, inducible RNAi would be advantageous: 1) production of large numbers of animals deficient for gene activities required for viability or reproduction, 2) generation of large populations of phenocopy mutants for biochemical analysis, and 3) effective gene inactivation in the nervous system. It is demonstrated herein that heritable inverted-repeat genes confer potent and specific gene inactivation for each of these

applications, significantly broadening the already remarkable utility of RNAi for *C. elegans* reverse genetics.

Many neurodegenerative disorders result from the aberrant expression and/or accumulation of proteins to toxic levels. The IR gene constructs of the invention may be utilized to inhibit the expression of such proteins thereby alleviating the pathological symptoms of the disorder.

In a similar fashion, the IR gene construct expression vectors of the invention may be engineered to inhibit the expression of viral proteins in infected cells. Such viruses include both plant and animal viruses.

The IR gene constructs also have utility for the treatment of neoplastic diseases. For example, the aberrant expression of oncogenes in certain cancers may be targeted for gene silencing using the compositions and methods of the invention. Such oncogenes include, without limitation, *ras*, *myc*, *myb*, *bcl-1*, *bcl-2*, *bcl-6*, *erb-a*, *erb-b*, *fgr*, *fos*, *src*, *lck*, and *lyn*,

The IR gene construct expression vectors of the invention are also suitable for the generation of transgenic knock-out mice. Such mice provide ideal in vivo models for studying the contribution of particular genes to embryonic development, growth and disease.

Finally, the IR gene construct expression vectors of the invention may be used to advantage to generate disease resistant plants. For example, geminiviruses are plant pathogens that infect a wide range of vegetable crops in tropical and subtropical regions with devastating consequences (Brown et al. (1992) Plant Disease, 76:220-225). Traditional breeding methods have failed to generate cultivars that are resistant to geminiviruses. Transformation of target crops with the

IR gene constructs of the invention encoding viral genes required for replication should effectively result in viral disease resistance.

5 **I. Definitions**

 The following definitions are provided to aid in understanding the subject matter regarded as the invention.

10 "Nucleic acid" or a "nucleic acid molecule" as used herein refers to any DNA or RNA molecule, either single or double stranded and, if single stranded, the molecule of its complementary sequence in either linear or circular form. In discussing nucleic acid molecules, a sequence or structure of a particular nucleic acid
15 molecule may be described herein according to the normal convention of providing the sequence in the 5' to 3' direction. With reference to nucleic acids of the invention, the term "isolated nucleic acid" is sometimes used. This term, when applied to DNA, refers to a DNA
20 molecule that is separated from sequences with which it is immediately contiguous in the naturally occurring genome of the organism in which it originated. For example, an "isolated nucleic acid" may comprise a DNA molecule inserted into a vector, such as a plasmid or
25 virus vector, or integrated into the genomic DNA of a prokaryotic or eukaryotic cell or host organism.

 When applied to RNA, the term "isolated nucleic acid" refers primarily to an RNA molecule encoded by an isolated DNA molecule as defined above. Alternatively,
30 the term may refer to an RNA molecule that has been sufficiently separated from other nucleic acids with which it would be associated in its natural state (i.e., in cells or tissues). An isolated nucleic acid (either DNA or RNA) may further represent a molecule produced
35 directly by biological or synthetic means and separated

from other components present during its production.

5 The terms "percent similarity", "percent identity" and "percent homology" when referring to a particular sequence are used as set forth in the University of Wisconsin GCG software program.

10 The phrase "inverted repeat gene" as used herein refers to an expression construct containing a promoter element operably linked in the 5' to 3' direction to a first coding sequence in a sense orientation which is in turn operably linked to a second sequence consisting of the first coding sequence in an anti-sense orientation. Alternatively, the first coding sequence may be in an antisense orientation and the second coding sequence may be in a sense orientation. The first and second coding
15 sequences range between 20 and 2500 nucleotides in length. Preferably the coding sequences may be between 100-300 nucleotides in length, 300-500 nucleotides in length, 500-800 nucleotides in length or 800-1500 nucleotides in length. Most preferably the first and
20 second coding sequences are about 1000 nucleotides in length. The expression construct also contains 3' regulatory regions which facilitate transcription of the inverted repeat gene in the targeted organism and the processing, expression, and translocation of its
25 transcript. The IR gene constructs of the invention may optionally comprise a spacer sequence between the first and second coding sequences. Such spacer regions may be between 300-1000 nucleotides in length. In certain embodiments, the spacer comprises an intronic region.

30 The term "functional" as used herein implies that the nucleic or amino acid sequence is functional for the recited assay or purpose.

The phrase "consisting essentially of" when referring to a particular nucleotide or amino acid
35 means a sequence having the properties of a given SEQ ID

No:. For example, when used in reference to an amino acid sequence, the phrase includes the sequence per se and molecular modifications that would not affect the basic and novel characteristics of the sequence.

5 A "replicon" is any genetic element, for example, a plasmid, cosmid, bacmid, phage or virus, that is capable of replication largely under its own control. A replicon may be either RNA or DNA and may be single or double stranded.

10 A "vector" is a replicon, such as a plasmid, cosmid, bacmid, phage or virus, to which another genetic sequence or element (either DNA or RNA) may be attached so as to bring about the replication of the attached sequence or element.

15 An "expression operon" refers to a nucleic acid segment that may possess transcriptional and translational control sequences, such as promoters, enhancers, translational start signals (e.g., ATG or AUG codons), polyadenylation signals, terminators, and the like, and which facilitate the expression of a
20 polypeptide coding sequence in a host cell or organism. Promoters may be inducible or constitutive. Inducible promoters include without limitation, heat shock promoter, metallothienine promoter, glucocorticoid
25 promoter. Constitutive promoters suitable for the practice of the present invention in worms include, without limitation, nervous system promoters, such as unc-119, mec-4, odr-4, muscle promoters, such as unc-54 and myo-2 and general promoters, such as act-1 and ben-
30 1. In higher organisms, promoters such as CMV are suitable. Other mammalian promoters are known to those of skill in the art and include for example, SV40, Mt promoter, glucocorticoid promoters.

35 When plants are targeted for gene silencing, the term "DNA construct" refers to genetic sequence used to

transform plants and generate progeny transgenic plants. These IR gene constructs may be administered to plants in a viral or plasmid expression vector. The biolistic process of transformation is preferred for practice of the present invention. Other methods of delivery such as *Agrobacterium* T-DNA mediated transformation and transformation using electroporation are also contemplated to be within the scope of the present invention.

In a preferred embodiment of the present invention, the associated plant promoter is a strong and non tissue- or developmental-specific plant promoter (e.g. a promoter that strongly expresses in many or all tissue types). Examples of such strong, "constitutive" promoters include, but are not limited to, the CaMV 35S promoter, the T-DNA mannopine synthetase promoter, and their various derivatives.

In another embodiment of the present invention, it may be advantageous to engineer a plant with a gene construct operably associating a tissue- or developmental-specific promoter with a sequence encoding the desired enzyme. For example, where expression in photosynthetic tissues and organs are desired, promoters such as those of the ribulose bisphosphate carboxylase (RUBISCO) genes or chlorophyll a/b binding protein (CAB) genes may be used; where expression in seed is desired, promoters such as those of the various seed storage protein genes may be used; where expression in nitrogen fixing nodules is desired, promoters such those of the leghemoglobin or nodulin genes may be used; where root specific expression is desired, promoters such as those encoding for root-specific glutamine synthetase genes may be used (see Tingey et al., 1987, EMBO J.6:1-9; Edwards et al., 1990, Proc. Nat. Acad. Sci. USA 87:3459-3463).

In an additional embodiment of the present invention, it may be advantageous to transform a plant with an IR gene construct expression vector operably associating an inducible promoter with a sequence encoding the IR gene construct. Examples of such promoters are many and varied. They include, but are not limited to, those of the heat shock genes, the defense responsive gene (e.g., phenylalanine ammonia lyase genes), wound induced genes (e.g., hydroxyproline rich cell wall protein genes), chemically-inducible genes (e.g., nitrate reductase genes, gluconase genes, chitinase genes, etc.), dark-inducible genes (e.g., asparagine synthetase gene (Coruzzi and Tsai, U.S. Pat. No. 5,256,558, Oct. 26, 1993, Gene Encoding Plant Asparagine Synthetase) to name just a few.

The plant IR gene construct expression vectors of the invention may also comprise 3' terminator sequences to stabilize the mRNA encoded by the construct. Such sequences include, without limitation, poly A sequences, and the os or nos 3' terminator sequence.

The term "probe" as used herein refers to an oligonucleotide, polynucleotide or nucleic acid, either RNA or DNA, whether occurring naturally as in a purified restriction enzyme digest or produced synthetically, which is capable of annealing with or specifically hybridizing to a nucleic acid with sequences complementary to the probe. A probe may be either single-stranded or double-stranded. The exact length of the probe will depend upon many factors, including temperature, source of probe and use of the method. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide probe typically contains 15-25 or more nucleotides, although it may contain fewer nucleotides. The probes herein are selected to be "substantially" complementary

to different strands of a particular target nucleic acid sequence. This means that the probes must be sufficiently complementary so as to be able to "specifically hybridize" or anneal with their respective target strands under a set of pre-determined conditions. Therefore, the probe sequence need not reflect the exact complementary sequence of the target. For example, a non-complementary nucleotide fragment may be attached to the 5' or 3' end of the probe, with the remainder of the probe sequence being complementary to the target strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the sequence of the target nucleic acid to anneal therewith specifically. The term "specifically hybridize" refers to the association between two single-stranded nucleic acid molecules of sufficiently complementary sequence to permit such hybridization under pre-determined conditions generally used in the art (sometimes termed "substantially complementary"). In particular, the term refers to hybridization of an oligonucleotide with a substantially complementary sequence contained within a single-stranded DNA or RNA molecule of the invention, to the substantial exclusion of hybridization of the oligonucleotide with single-stranded nucleic acids of non-complementary sequence.

The term "primer" as used herein refers to an oligonucleotide, either RNA or DNA, either single-stranded or double-stranded, either derived from a biological system, generated by restriction enzyme digestion, or produced synthetically which, when placed in the proper environment, is able to functionally act as an initiator of template-dependent nucleic acid synthesis. When presented with an appropriate nucleic

acid template, suitable nucleoside triphosphate precursors of nucleic acids, a polymerase enzyme, suitable cofactors and conditions such as a suitable temperature and pH, the primer may be extended at its 3' terminus by the addition of nucleotides by the action of a polymerase or similar activity to yield an primer extension product. The primer may vary in length depending on the particular conditions and requirement of the application. For example, in diagnostic applications, the oligonucleotide primer is typically 15-25 or more nucleotides in length. The primer must be of sufficient complementarity to the desired template to prime the synthesis of the desired extension product, that is, to be able anneal with the desired template strand in a manner sufficient to provide the 3' hydroxyl moiety of the primer in appropriate juxtaposition for use in the initiation of synthesis by a polymerase or similar enzyme. It is not required that the primer sequence represent an exact complement of the desired template. For example, a non-complementary nucleotide sequence may be attached to the 5' end of an otherwise complementary primer. Alternatively, non-complementary bases may be interspersed within the oligonucleotide primer sequence, provided that the primer sequence has sufficient complementarity with the sequence of the desired template strand to functionally provide a template-primer complex for the synthesis of the extension product.

All amino-acid residue sequences represented herein conform to the conventional left-to-right amino-terminus to carboxy-terminus orientation.

The term "substantially pure" refers to a preparation comprising at least 50-60% by weight of a given material (e.g., nucleic acid, oligonucleotide, protein, etc.). More preferably, the preparation

comprises at least 75% by weight, and most preferably 90-95% by weight of the given compound. Purity is measured by methods appropriate for the given compound (e.g. chromatographic methods, agarose or polyacrylamide gel electrophoresis, HPLC analysis, and the like).

The terms "transform", "transfect", "transduce", shall refer to any method or means by which a nucleic acid is introduced into a cell or host organism and may be used interchangeably to convey the same meaning. Such methods include, but are not limited to, transfection, electroporation, microinjection, PEG-fusion and the like.

The introduced nucleic acid may or may not be integrated (covalently linked) into nucleic acid of the recipient cell or organism. In bacterial, yeast, plant and mammalian cells, for example, the introduced nucleic acid may be maintained as an episomal element or independent replicon such as a plasmid. Alternatively, the introduced nucleic acid may become integrated into the nucleic acid of the recipient cell or organism and be stably maintained in that cell or organism and further passed on or inherited to progeny cells or organisms of the recipient cell or organism. In other manners, the introduced nucleic acid may exist in the recipient cell or host organism only transiently.

A "clone" or "clonal cell population" is a population of cells derived from a single cell or common ancestor by mitosis.

A "cell line" is a clone of a primary cell or cell population that is capable of stable growth *in vitro* for many generations.

A "disease related protein may be a viral, bacterial or aberrant endogenously produced protein associated with a particular disease phenotype. Such human proteins include, without limitation, those set

forth in Table I below:

TABLE I

Increased dosage/Gain-of-function disease genes in humans

1.	>gi	6681203	ref	NP_031894.1	dystrophin, muscular dystrophy [Mus musculus]
2.	>gi	6995996	ref	NP_000483.2	cystic fibrosis TM conductance regulator
3.	>gi	4753163	ref	NP_002102.2	huntingtin [Homo sapiens]
4.	>gi	4502167	ref	NP_000475.1	amyloid beta (A4) precursor protein
5.	>gi	2135246	pir	A56993	presenilin 2 - human
6.	>gi	4506435	ref	NP_000312.1	retinoblastoma 1 (osteosarcoma) [Homo sapiens]
7.	>gi	1082578	pir	S50830	Machado-Joseph disease MJD1a protein - human
8.	>gi	1709040	sp	P54252	MJD1_HUMAN MACHADO-JOSEPH DISEASE PROTEIN 1
9.	>gi	3063388	dbj	BAA25751.1	Parkin [Homo sapiens]
10.	>gi	4506113	ref	NP_000302.1	prion protein (p27-30) [Homo sapiens]
11.	>gi	2498924	sp	Q16637	SMN1_HUMAN SURVIVAL MOTOR NEURON PROTEIN 1
12.	>gi	4507891	ref	NP_000542.1	von Hippel-Lindau syndrome tumor suppressor
13.	>gi	4507091	ref	NP_000335.1	survival of motor neuron 1, telomeric
14.	>gi	6166210	sp	Q92902	HFS_HUMAN HERMANSKY-PUDLAK SYNDROME PROTEIN
15.	>gi	2228793	gb	AAC51731.1	Jagged1 [Homo sapiens]
16.	>gi	904119	gb	AAB46416.1	S182 gene product, Alzheimer Disease Chr. 14
17.	>gi	950348	gb	AAC42012.1	E5-1 protein Alzheimer Disease Chr. 1
18.	>gi	4557365	ref	NP_000048.1	Bloom syndrome protein [Homo sapiens]
19.	>gi	4502839	ref	NP_000072.1	Chediak-Higashi syndrome 1 [Homo sapiens]
20.	>gi	6166193	sp	Q16595	FRDA_HUMAN FRATAXIN (FRIEDREICH'S ATAXIA PROTEIN)
21.	>gi	6166210	sp	Q92902	HFS_HUMAN HERMANSKY-PUDLAK SYNDROME PROTEIN
22.	>gi	4504455	ref	NP_000183.1	Holt-Oram syndrome [Homo sapiens]
23.	>gi	4557683	ref	NP_000207.1	Kallmann syndrome 1 protein [Homo sapiens]
24.	>gi	7531135	sp	Q12809	HERG_HUMAN VOLTAGE-GATED POTASSIUM CHANNEL
25.	>gi	400664	sp	Q01968	OCRL_HUMAN LOWE'S OCULOCEREBRORENAL SYNDROME PROTEIN
26.	>gi	1709040	sp	P54252	MJD1_HUMAN MACHADO-JOSEPH DISEASE PROTEIN 1
27.	>gi	2135606	pir	I39294	McLeod syndrome-associated protein XK - human
28.	>gi	4502321	ref	NP_000043.1	ATPase, Cu++ transporting, (Menkes syndrome) [Homo sapiens]
29.	>gi	5729770	ref	NP_000382.3	ceroid-lipofuscinosis, neuronal 2, [Homo sapiens]
30.	>gi	4557803	ref	NP_000262.1	Niemann-Pick disease, type C1 [Homo sapiens]
31.	>gi	4505339	ref	NP_002476.1	Nijmegen breakage syndrome 1; nibrin [Homo sapiens]
32.	>gi	4505833	ref	NP_000287.1	polycystic kidney disease 1 [Homo sapiens]
33.	>gi	3126905	gb	AAC16004.1	polycystic kidney disease type II protein
34.	>gi	4507091	ref	NP_000335.1	survival of motor neuron 1, [Homo sapiens]
35.	>gi	4506793	ref	NP_000323.1	ataxin 1; spinocerebellar ataxia 1
36.	>gi	4506795	ref	NP_002964.1	ataxin 2; spinocerebellar ataxia 2
37.	>gi	4506797	ref	NP_000324.1	ataxin 7; spinocerebellar ataxia 7 [Homo sapiens]
38.	>gi	4507891	ref	NP_000542.1	von Hippel-Lindau syndrome tumor suppressor
39.	>gi	482301	pir	A38080	Wilms tumor susceptibility protein WT1 - human
40.	>gi	7513430	pir	A55197	Wiskott-Aldrich syndrome protein WASP - human
41.	>gi	5174749	ref	NP_005996.1	Wolfram syndrome [Homo sapiens]
42.	>gi	6094278	sp	O60880	SH2A DOMAIN PROTEIN 1A (DUNCAN'S DISEASE SH2-PROTEIN)
43.	>gi	4502889	ref	NP_000077.1	ceroid-lipofuscinosis, Spielmeier-Vogt disease
44.	>gi	189356	gb	AAA59964.1	Lowe Syndrome
45.	>gi	515873			Membrane transport protein, McLeod Syndrome
46.	>gi	34705	emb	CAA49145.1	Menkes Disease
47.	>gi	307177	gb	AAA36206.1	protein kinase, Myotonic Dystrophy
48.	>gi	292292	gb	AAA36212.1	Neurofibromatosis, Type 2
49.	>gi	1163234	gb	AAA91041.1	Dpc4, Pancreatic Carcinoma
50.	>gi	1314871	gb	AAC50481.1	retinitis pigmentosa GTPase regulator
51.	>gi	1237181	gb	AAA98132.1	glypican, Simpson-Golabi- Behmel syndrome
52.	>gi	624186	gb	AAA66242.1	survival motor neuron
53.	>gi	1737213	gb	AAC52047.1	neuronal apoptosis inhibitory protein [Homo sapiens]
54.	>gi	529662	emb	CAA55793.1	ataxin-1 [Homo sapiens] Spinocerebral Ataxia
55.	>gi	731120	sp	P40337	VHL_HUMAN VON HIPPEL-LINDAU DISEASE TUMOR SUPPRESSOR (G7)
56.	>gi	435421	gb	AAA03628.1	PAX-3 Waardenburg Syndrome

II. Preparation of Nucleic Acid Molecules Encoding the Inverted Repeat Genes of the Invention

Nucleic acid molecules comprising the inverted repeat genes of the invention may be prepared by two general methods: (1) synthesis from appropriate

nucleotide triphosphates, or (2) isolation from biological sources. Both methods utilize protocols well known in the art. The availability of nucleotide sequence information for genes targeted for knock-out enables preparation of an isolated nucleic acid molecule of the invention by oligonucleotide synthesis. Synthetic oligonucleotides may be prepared by the phosphoramidite method employed in the Applied Biosystems 38A DNA Synthesizer or similar devices. The resultant construct may be purified according to methods known in the art, such as high performance liquid chromatography (HPLC). Long, double-stranded polynucleotides, such as a DNA molecule of the present invention, must be synthesized in stages, due to the size limitations inherent in current oligonucleotide synthetic methods. Thus, for example, a 1.9 kb double-stranded molecule may be synthesized as several smaller segments of appropriate complementarity. Complementary segments thus produced may be annealed such that each segment possesses appropriate cohesive termini for attachment of an adjacent segment. Adjacent segments may be ligated by annealing cohesive termini in the presence of DNA ligase to construct an entire 1.9 kb double-stranded molecule. A synthetic DNA molecule so constructed may then be cloned and amplified in an appropriate vector.

Nucleic acid sequences encoding the inverted repeat genes of the invention may be isolated from appropriate biological sources using methods known in the art. In one embodiment, a clone is amplified from a DNA expression library of from the desired species of origin. Suitable primers for this purpose are derived from sequences within the gene targeted for silencing. Such primers may be between 15 and 40 nucleotides in length. Alternative approaches for obtaining DNA for

the inverted repeat genes of the invention, include cloning the inverted repeat fragments directly or chemically synthesizing the entire inverted repeat gene. In accordance with the present invention, nucleic acids having the appropriate level of sequence homology with the protein coding region of genes targeted for silencing may be identified by using hybridization and washing conditions of appropriate stringency. For example, hybridizations may be performed, according to the method of Sambrook et al., Molecular Cloning, Cold Spring Harbor Laboratory (1989), using a hybridization solution comprising: 5X SSC, 5X Denhardt's reagent, 1.0% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.05% sodium pyrophosphate and up to 50% formamide. Hybridization is carried out at 37-42 C for at least six hours. Following hybridization, filters are washed as follows: (1) 5 minutes at room temperature in 2X SSC and 1% SDS; (2) 15 minutes at room temperature in 2X SSC and 0.1% SDS; (3) 30 minutes-1 hour at 37 C in 1X SSC and 1% SDS; (4) 2 hours at 42-65 C in 1X SSC and 1% SDS, changing the solution every 30 minutes.

One common formula for calculating the stringency conditions required to achieve hybridization between nucleic acid molecules of a specified sequence homology (Sambrook et al., 1989) is as follows: $T_m = 81.5^{\circ}\text{C} + 16.6\text{Log} [\text{Na}^+] + 0.41(\% \text{G+C}) - 0.63 (\% \text{formamide}) - 600/\text{\#bp in duplex}$. As an illustration of the above formula, using $[\text{Na}^+] = [0.368]$ and 50% formamide, with GC content of 42% and an average probe size of 200 bases, the T_m is 57°C. The T_m of a DNA duplex decreases by 1 - 1.5°C with every 1% decrease in homology. Thus, targets with greater than about 75% sequence identity would be observed using a hybridization temperature of 42°C.

Rather than direct cloning of genes targeted for

silencing, an alternative approach entails identification of target genes by homology searches in available the available nucleic acid databases such as Genbank.

5 The inverted repeat genes of the present invention may be maintained as DNA in any convenient cloning vector. In a preferred embodiment, clones are maintained in a plasmid cloning/expression vector, such as pBluescript (Stratagene, La Jolla, CA), which is
10 propagated in a suitable *E. coli* host cell. Other vectors suitable for the practice of the present invention, include, without limitation, pBlue/TOPO (Invitrogen), PCR-Blunt-TOPO (Invitrogen) and the pCDNA series from Invitrogen.

15
III. Selection and Preparation of Expression vectors containing the IR gene constructs of the invention

Selection of a suitable sequence targeted for knock-out depends on knowledge of the nucleotide
20 sequence of the target mRNA, or gene from which the mRNA is transcribed. Although targeting to mRNA is preferred and exemplified in the description below, it will be appreciated by those skilled in the art that other forms of nucleic acid, such as pre-mRNA or genomic DNA, may
25 also be targeted.

Double-stranded IR transcripts should correspond to regions present in the transcript encoding the targeted protein. Such sequences include, but are not limited to
30 5' untranslated regions, coding regions and the 3' untranslated regions.

Various genetic regulatory control elements may be incorporated into the expression vectors containing the IR gene constructs of the invention to facilitate propagation in both eucaryotic and procaryotic cells.

35 Different promoters may be utilized to drive expression

of the IR gene construct sequences, the cytomegalovirus immediate early promoter being preferred for use in humans as it promotes a high level of expression of downstream sequences. Polyadenylation signal sequences are also utilized to promote mRNA stability. Sequences preferred for use in human cells include, but are not limited to, bovine growth hormone polyadenylation signal sequences or thymidine kinase polyadenylation signal sequences. Antibiotic resistance markers are also included in these vectors to enable selection of transformed cells. These may include, for example, genes that confer hygromycin, neomycin or ampicillin resistance.

A variety of different vectors are available for use in the methods of the invention. These include without limitation, those set forth in Table II. The listed vector have been utilized to express the indicated proteins. Conventional molecular biological techniques may be utilized to replace the protein coding sequence with the IR gene constructs of the invention.

TABLE II

VECTORS FOR USE IN THE METHODS OF THE INVENTION

Name	Description
pACCMVpLmPl(-)loxP-SSP	Adenoviral shuttle plasmid with unique restriction tag, SmaI, SfiI, PmeI, CMV promoter, pUC19 polylinker, mPl splicing signal/poly A, loxP
pACCMVpLpA(-)loxP	Adenoviral shuttle plasmid, CMV promoter, pUC19 polylinker, SV40 splice/polyA, loxP
PACCMVpLPA(-)loxP-SSP	Adenoviral shuttle plasmid with unique restriction tag, SmaI, SfiI, PmeI, CMV promoter, pUC19 polylinker, SV40 splice/polyA, loxP

	pACpL+loxP	Adenoviral shuttle plasmid, no promoter
5	pACpL +loxP-SSP	Adenoviral shuttle plasmid, no promoter, SwaI, SfiI, PmeI unique site cluster
10	pAd-HSV	tkHSV tk, thymidine kinase, pAD BglII
	pAdBgI II	Ampicillin Resistance, Recombinant Adenovirus
15	pAdEF1 alpha loxP	Adenovirus, EF 1 alpha promoter, loxP
	pAdMCSlacZ	multiple cloning sites, lacZ gene
20	pAdMCSloxP	Adenoviral shuttle vector, polylinker, loxP
	pAdMCSpA	multiple cloning sites, SV40 PolyA signal
25	pAdMCSpA/lacZ	multiple cloning sites, lacZ gene, SV40 poly(A) signal
30	pAdRSV4	RSV promoter, multiple cloning sites, SV40 poly(A)
	pNGVL1	PstI, SalI, HindIII, EcoRV, BglII polylinker, kanamycin resistance
35	pNGVL1-CAT	chloramphenicol transferase
	pNGVL1-hGM-CSF	human granulocyte-monocyte colony stimulating factor
40	pNGVL1-hpAP	human placental alkaline phosphatase
45	pNGVL1-mGM-CSF	mouse granulocyte-monocyte colony stimulating factor
	pNGVL1-ntbeta-gal	nuclear targeted beta-galactosidase
50	pNGVL1-tk	thymidine kinase
	pNGVL2	polylinker deleted, kanamycin

		resistance
	pNGVL3	12 site polylinker, kanamycin resistance
5	pNGVL3-4070a-env	Amphotropic 4070A virus env.
	pNGVL3-gag-pol	retrovirus gag-pol helper plasmid, kanamycin resistant
10	pNGVL3-hFL	human full length Flt3 ligand cDNA
	pNGVL3-hFLex	human Flt3 ligand, secreted
15	pNGVL3-hIL10	human interleukin 10
	pNGVL3-hIL12	human interleukin-12, internal ribosome entry site
20	pNGVL3-hIL15	human interleukin- 15
	pNGVL3-hIL2	human interleukin-2
25	pNGVL3-hIL2/IL15	human IL2-IL15 fusion
	pNGVL3-hIL4	human interleukin 4
	pNGVL3-hIL7	human interleukin 7
30	pNGVL3-mFL	mouse FLT3 ligand
	pNGVL3-mFLex	Extracellular domain of mouse FLT3 ligand
35	pNGVL3-mIL10	mouse interleukin 10
	pNGVL3-mIL12	mouse interleukin 12, internal ribosome entry site
40	pNGVL3-mIL15	mouse interleukin- 15
	pNGVL3-mIL2	Mouse interleukin-2
45	pNGVL3-mIL4	mouse interleukin 4
	pNGVL3-mIL7	mouse interleukin 7
50	pNGVL3-shIL15R	soluble human interleukin 15 receptor
	pNGVL3-smIL15R	soluble mouse interleukin- 15

		receptor
	pNGVL4a	immunostimulatory sequence
5	pNGVL4b	immunostimulatory sequence
	pNGVL5	IL2 secretory signal peptide
	pNGVL6a	IL2 secretion signal peptide
10	pNGVL7	pNGVL7, CMV, tpa
	RVNL3(+)	CMV promoter, ATG(-), non- episomal, retrovirus
15		vector

IV. Uses of Nucleic Acids Encoding Inverted Repeat

Genes

20 Gene silencing provides a powerful technique for
the elucidation of molecular and biochemical mechanisms
associated with homeostasis, growth and development.
The inverted repeat genes of the invention may be used
to advantage to "knock out" the activity of any target
25 gene, provided the sequence of the target gene is known.
The inverted repeat gene constructs have been designed
such that they are both inducible and heritable.
Expression of the inverted repeat genes of the invention
driven from strong inducible promoters facilitates the
30 formation of a double stranded "snap back" RNA
endogenously, thereby abrogating functional expression
of the target gene.

 Gene expression manipulation is extremely important
to the pharmaceutical industry. Beneficial uses of this
35 invention include specific gene inactivation for the
investigation of gene function and reverse genetic
studies. When *C. elegans* is used as the target
organism, the compositions and methods of the invention
facilitate the production of phenocopy mutants which can
40 be induced also in offspring. Thus the invention
provides for the production of large populations of

nematodes that can be subjected to gene inactivation at any time during growth and development which in turn may be used to advantage for drug screening, large scale genetic mutant assessment, and biochemical studies.

5 The invention also provides for disruption of gene activity, markedly improving current protocols which appear to be ineffective in neuronal "knock out". The invention also provides for large scale preparations for analysis of the RNAi mechanism itself.

10 Additionally, this protocols described herein may be used to inactivate or disrupt gene activity in any organism. Any organism which may be transformed with exogenous DNA corresponding to a target gene having a defined promoter may be subjected to gene silencing
15 using the compositions and methods of the present invention. Such organisms include, without limitation, yeast, Dictostelium, drosophila, mice, insects, plants, human cells and other nematodes. Such methods facilitate an analysis of specific gene function by
20 phenocopy knockout. Additionally, other harmful or potentially harmful gene expression may be inhibited or prevented in accordance with the invention. Such genes include by way of illustration, genes required for oncogenesis, productive HIV infection and genes required
25 for successful infection by a variety of pathogenic organisms.

The availability of sequence information encoding nucleic acids targeted for gene silencing enables the production of strains of laboratory mice carrying the IR
30 gene constructs of the invention. Such mice provide an in vivo model for assessing growth development and disease. The compositions and methods provided herein enables the production of knockout mice in which the endogenous gene corresponding to the IR gene construct
35 has been specifically inactivated. Methods of

introducing IR gene construct expression vectors in laboratory mice are known to those of skill in the art. Three common methods include: 1. integration of retroviral vectors encoding the foreign gene of interest into an early embryo; 2. injection of DNA into the pronucleus of a newly fertilized egg; and 3. the incorporation of genetically manipulated embryonic stem cells into an early embryo. Production of the transgenic mice described above will facilitate the molecular elucidation of the role predetermined target genes play in embryonic development and disease.

A "transgenic animal" is any animal containing one or more cells bearing genetic information altered or received, directly or indirectly, by deliberate genetic manipulation at the subcellular level, such as by targeted recombination or microinjection or infection with recombinant virus. The term "transgenic animal" is not meant to encompass classical cross-breeding or in vitro fertilization, but rather is meant to encompass animals in which one or more cells are altered by or receive a recombinant DNA molecule. This molecule may be specifically targeted to a defined genetic locus, be randomly integrated within a chromosome, or it may be extrachromosomally replicating DNA. The term "germ cell line transgenic animal" refers to a transgenic animal in which the genetic alteration or genetic information was introduced into a germ line cell, thereby conferring the ability to transfer the genetic information to offspring. If such offspring, in fact, possess some or all of that alteration or genetic information, then they, too, are transgenic animals.

The DNA used for altering expression of a target gene may be obtained by a wide variety of techniques that include, but are not limited to, isolation from genomic sources, preparation of cDNAs from isolated mRNA

templates, direct synthesis, or a combination thereof. A type of target cell for transgene introduction is the embryonal stem cell (ES). ES cells may be obtained from pre-implantation embryos cultured in vitro (Evans et al., (1981) Nature **292**:154-156; Bradley et al., (1984) Nature **309**:255-258; Gossler et al., (1986) Proc. Natl. Acad. Sci. **83**:9065-9069). Transgenes can be efficiently introduced into the ES cells by standard techniques such as DNA transfection or by retrovirus-mediated transduction. The resultant transformed ES cells can thereafter be combined with blastocysts from a non-human animal. The introduced ES cells thereafter colonize the embryo and contribute to the germ line of the resulting chimeric animal.

One approach to the problem of determining the contributions of individual genes and their expression products is to use IR gene constructs to selectively inactivate the wild-type gene in totipotent ES cells (such as those described above) and then generate transgenic mice. The use of gene-targeted ES cells in the generation of gene-targeted transgenic mice was described, and is reviewed elsewhere (Frohman et al., (1989) Cell **56**:145-147; Bradley et al., (1992) Bio/Technology **10**:534-539).

Techniques are available to inactivate or alter any genetic region to a mutation desired by using targeted homologous recombination to insert specific changes into chromosomal alleles. However, in comparison with homologous extrachromosomal recombination, which occurs at a frequency approaching 100%, homologous plasmid-chromosome recombination was originally reported to only be detected at frequencies between 10^{-6} and 10^{-3} . Nonhomologous plasmid-chromosome interactions are more frequent occurring at levels 10^5 -fold to 10^2 -fold greater than comparable homologous insertion.

To overcome this low proportion of targeted recombination in murine ES cells, various strategies have been developed to detect or select rare homologous recombinants. One approach for detecting homologous alteration events uses the polymerase chain reaction (PCR) to screen pools of transformant cells for homologous insertion, followed by screening of individual clones. Alternatively, a positive genetic selection approach has been developed in which a marker gene is constructed which will only be active if homologous insertion occurs, allowing these recombinants to be selected directly. One of the most powerful approaches developed for selecting homologous recombinants is the positive-negative selection (PNS) method developed for genes for which no direct selection of the alteration exists. The PNS method is more efficient for targeting genes which are not expressed at high levels because the marker gene has its own promoter. Non-homologous recombinants are selected against by using the Herpes Simplex virus thymidine kinase (HSV-TK) gene and selecting against its nonhomologous insertion with effective herpes drugs such as gancyclovir (GANC) or (1-(2-deoxy-2-fluoro-B-D arabinofluranosyl)-5-iodouracil, (FIAU). By this counter selection, the number of homologous recombinants in the surviving transformants can be increased.

Methods of use for the transgenic mice of the invention are also provided herein. Therapeutic agents for the treatment or prevention of disease may be screened in studies using transgenic mice harboring the IR gene constructs of the invention.

As mentioned previously, the IR gene construct expression vectors of the invention may be used for gene silencing in any organism which may be targeted with exogenous DNA. Uses of the expression vectors for the

treatment of human and plant diseases is also exemplified herein.

5 **V. Administration of Plasmid Vectors Producing the IR genes of the invention**

 The IR gene construct containing expression vectors as described herein are generally administered to a patient as a pharmaceutical preparation. The term
10 "patient" as used herein refers to human or animal subjects.

 The pharmaceutical preparation comprising the IR gene construct expression vector of the invention is conveniently formulated for administration with a
15 acceptable medium such as water, buffered saline, ethanol, polyol (for example, glycerol, propylene glycol, liquid polyethylene glycol and the like), dimethyl sulfoxide (DMSO), oils, detergents, suspending agents or suitable mixtures thereof. The concentration
20 of expression vector in the chosen medium will depend on the hydrophobic or hydrophilic nature of the medium, as well as the length and other properties of the vector molecule. Solubility limits may be easily determined by one skilled in the art.

25 As used herein, "biologically acceptable medium" includes any and all solvents, dispersion media and the like which may be appropriate for the desired route of administration of the pharmaceutical preparation, as exemplified in the preceding paragraph. The use of such
30 media for pharmaceutically active substances is known in the art. Except insofar as any conventional media or agent is incompatible with the IR gene construct expression vectors to be administered, its use in the pharmaceutical preparation is contemplated.

35 Selection of a suitable pharmaceutical preparation

depends upon the method of administration chosen. For example, IR gene construct expression vectors may be administered by direct injection into the region of the brain containing the targeted cell type. In this instance, a pharmaceutical preparation comprises the IR gene construct expression vector dispersed in a medium that is compatible with cerebrospinal fluid. In a preferred embodiment, artificial cerebrospinal fluid (148 mM NaCl, 2.9 mM KCl, 1.6 mM MgCl₂ · 6H₂O, 1.7 mM CaCl₂, 2.2 mM dextrose) is utilized, and IR gene construct expression vectors are provided directly to neurons by intraventricular injection.

IR gene construct expression vectors for use in gene silencing may also be administered parenterally by intravenous injection into the blood stream, or by subcutaneous, intramuscular or intraperitoneal injection. Pharmaceutical preparations for parenteral injection are commonly known in the art. If parenteral injection is selected as a method for administering the IR gene construct expression vector, steps must be taken to ensure that sufficient amounts of the molecules reach their target cells to exert a biological effect. The lipophilicity of the IR gene construct expression vectors, or the pharmaceutical preparation in which they are delivered may have to be increased so that the molecules can cross the blood-brain barrier to arrive at their target locations. Furthermore, the IR gene construct expression vectors may have to be delivered in a cell-targeted carrier so that sufficient numbers of molecules will reach the target cells. Methods for increasing the lipophilicity of a molecule are known in the art, and include the addition of lipophilic groups to the IR gene construct expression vector.

Several techniques have been used to increase the stability, cellular uptake and biodistribution of DNA

expression vectors. The expression vector of the present invention may be encapsulated in a lipophilic, targeted carrier, such as a liposome. One technique is to use as a carrier for the expression vector a
5 liposomal preparation containing the cationic lipid N-[1-(2,3-dioleyloxy)propyl]-N,N,N-trimethyl ammonium chloride (DOTMA; lipofectin).

The vectors of the present invention may be complexed to liposomes. To further facilitate targeting
10 of the IR gene construct expression vector, liposomes may be "studded" with antibodies specific for certain regions of the brain (Leserman et al., (1980) Nature 288:604). In a preferred embodiment, cationic liposomes are complexed with (1) the IR gene construct expression
15 vector; and (2) antibodies specific for the desired region of the brain. Vector containing antibody-studded-liposome complexes are expected not only to be targeted and specifically expressed in the desired regions of the brain, but also to be expressed for
20 indefinitely.

The pharmaceutical preparation is formulated in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form, as used herein, refers to a physically discrete unit of the
25 pharmaceutical preparation appropriate for the patient undergoing treatment. Each dosage should contain a quantity of active ingredient calculated to produce the desired effect in association with the selected pharmaceutical carrier. Procedures for determining the
30 appropriate dosage unit are well known to those skilled in the art.

The pharmaceutical preparation comprising the IR gene construct expression vector may be administered at appropriate intervals, for example, twice a day until
35 the pathological symptoms are reduced or alleviated,

after which the dosage may be reduced to a maintenance level. The appropriate interval in a particular case would normally depend on the condition of the patient.

When performing gene silencing in plants, the IR gene construct expression vector is delivered to plant cells using biolistic or Agrobacterium mediated DNA transfer. Selection and propagation of transformed plant cells is performed according to methods well known to those of ordinary skill in the art.

The following protocols are provided to facilitate the practice of the present invention.

Nematode strains. *C. elegans* strains were reared and maintained as described²¹. We constructed transgenic lines by injection of plasmid DNAs each at 100ng/ μ l using standard protocols²². In all experiments we used plasmid pRF4²³, which harbors a dominant *rol-6* allele that causes a readily distinguished roller phenotype in transgenic animals, as a co-transformation marker.

Construction of inverted repeat genes. We PCR amplified exon-rich genomic DNA (or cDNA) using two primers that introduce unique restriction sites at the fragment ends. We digested the amplified fragment with one of the enzymes and ligated to generate an inverted repeat (outlined in Fig. 2b). We then digested with the other enzyme, the restriction site for which is now positioned at the IR fragment ends, and ligated into CIAP-treated vector pPD49.78²², which includes the *hsp16-2* promoter and the 3' untranslated region of muscle myosin *unc-54*. The cDNA and genomic DNA we amplified for RNAi ranged from .58-1.45 kb in length. Alternative cloning strategies include: 1) digestion at two naturally

occurring restriction sites to excise the gene fragment of interest with subsequent two-step ligation as above, or 2) direct tri-molecular ligation of the doubly digested fragment into CIAP-treated vector previously linearized with one of the enzymes at the fragment end. In an alternative embodiment spacer loops are included between the inverted repeat gene segments. We found the efficiency of cloning inverted repeats to be acceptable in the *E. coli* DH5 strain (in general, a few per hundred candidates screened) and relatively high in the *E. coli* SURE strain (Stratagene), a bacterial host tolerant of inverted repeats (about 1/20 candidate constructs correct). The *hsp16-2_punc-8(IR)* construct, however, proved highly difficult to generate (1000 candidates screened, 0.58 kb of cDNA sequence in the repeat) for reasons that are not clear. Slower growing bacterial transformant colonies appear to have an enhanced chance of harboring the IR gene. The yield of plasmid DNA from IR genes harbored in *E. coli* DH5 strain is low (about 3-5 µg per 50 ml culture); when the SURE strain is the host, yields are improved (80-100 µg per 50 ml culture). While this method relates to PCR amplification of the target genes, it will be appreciated by those of skill in the art that other methods for obtaining the DNA for the inverted repeat genes of the invention are available. These include direct synthesis of the target gene on a DNA synthesizer and direct cloning using conventional hybridization and DNA isolation procedures.

RNA interference assays. For standard RNAi, we prepared dsRNA from cDNAs or coding sequence-rich genomic DNAs, .58-1.2 kb in length are injected into N2 adults/group as described¹. We scored progeny born to injected adults (10 adults per group) 12 hours or more after injection

(older progeny exhibit a much lower phenocopy rate). For genetically directed RNAi mediated by expression of inverted repeat genes, we selected 50 transgenic roller L4s from lines harboring various *hsp-16_p(IR)* constructs plus co-transformation plasmid pRF4²³ (array transmission frequency >60%) and reared continuously at 20 °C (non-heat shock) or heat shocked for 4 hours at 35 °C, before returning to 20 °C. Progeny of these animals were scored for phenotypes of interest at embryonic or larval stages as appropriate; behavioral assays and phenotypic analysis as indicated in Table 3 and Figure legends. On average at least half of lines for a given gene assayed conferred potent interference upon heat-activation.

The following examples are provided to illustrate various embodiments of the invention. They are not intended to limit the invention in any way.

EXAMPLE I

To test the feasibility of specific gene disruption via *in vivo* expression of double stranded RNA, we constructed transgenic nematodes that synthesize hairpin ds RNA³ from IR genes under the control of the strong heat shock-inducible promoter, *hsp16-2*⁶⁻⁸ (Fig. 2). We first compared effects of conventional RNAi via injection of dsRNA, expression of sense and antisense genes, and *in vivo* production of dsRNA using *C. elegans* predicted gene C37A2.5, an essential gene required for progression past the L2 larval stage (N. Tavernarakis, S. Wang, M., Driscoll, unpublished observations). Conventional RNAi via injection of C37A2.5 dsRNA¹ produces a high yield of L2 stage-arrested F1 progeny (Table 3). Expression of the antisense strand, which

can be an effective method for specific gene inactivation⁹, confers a modest percentage of phenocopy progeny, whereas expression of the sense stand is ineffective. To test *in vivo* RNAi, we heat-shocked young adults of transgenic lines harboring extrachromosomal *hsp16-2_pC37A2.5(IR)*. *In vivo* promoter-driven RNAi proved effective in reproducing the C37A2.5 null phenotype, with efficiencies approaching that of direct injection of dsRNA (Table 3). Likewise, promoter-driven RNAi efficiently disrupted the Mi-2 chromatin remodeling homolog F2612.7¹⁰ to phenocopy the sterile phenotype of a deletion of this gene (Table 1). We conclude that *in vivo* driven RNAi can be effective and that this technique should enable convenient generation of large populations of phenocopy mutants, even when development or reproduction is blocked.

Table 3.
***In vivo* dsRNA interference**

Gene disruption approach	Trial/Line 1	Trial/Line 2	Trial/Line 3	Trial/Line 4
dsRNA C37A2.5 injected	94±8	89±4	97±5	89±7
pPD49.78 (<i>hsp16-2_p</i> alone) + heat shock	0	0	0	0
<i>hsp16-2_pC37A2.5 sense</i> + heat shock	0	0	0	0
<i>hsp16-2_pC37A2.5 antisense</i> + heat shock	9±4	9±4	11±6	—
<i>hsp16-2_pC37A2.5(IR)</i> - heat shock	0	0	0	0
<i>hsp16-2_pC37A2.5(IR)</i> + heat shock	67±3	79±6	84±5	56±7
<i>hsp16-2_pF26F12.7(IR)</i> - heat shock	1±0.9	2±1	1±0.9	3±1.3
<i>hsp16-2_pF26F12.7(IR)</i> + heat shock	58±4	59±5	75±8	82±6
ds <i>mec-4</i> RNA injected	12±7	19±5	15±6	—
<i>hsp16-2_pmec-4(IR)</i> - heat shock	0	0	0	—

	<i>hsp16-2_pmec-4(IR)</i> + heat shock	58±4	60±7	61±8	—
5	ds <i>unc-8</i> RNA injected	0	0.8±.01	0	0
	<i>hsp16-2_punc-8(IR)</i> - heat shock	0	0	0	0
	<i>hsp16-2_punc-8(IR)</i> + heat shock	17±3	11±5	14±2	13±3

Results for four injection trials using conventional RNAi or heat shock induced in vivo RNAi in 4 transgenic lines (unless otherwise noted) are indicated. In all experiments, at least 100 animals were scored per experimental trial. Gene C37A2.5 is required for developmental progression past the L2 stage. Numbers indicate the percentage of F1 progeny arrested at the L2 stage ± SD. Co-expression of sense and antisense genes, which can be effective²⁴, was not tested. Deletion of chromatin remodeling gene homolog F26F12.7 causes sterility (S. Wang and M. Driscoll, unpublished). Treated progeny of transgenic lines harboring *hsp16-2_pF26F12.7(IR)* were scored for % that fail to develop into fertile adults. A similar strategy for in vivo disruption of a second MI-2 homolog, T14G8.1, yielded 59% and 72% sterile in progeny of two lines scored after heat shock (data not shown). *mec-4* is expressed in six mechanosensory neurons and is required for touch sensitivity. ds *mec-4* RNA or plasmid *hsp16-2_pmec-4(IR)* was introduced into wild type animals and progeny were scored for touch insensitivity. *unc-8(n491)* is a dominant gain-of-function mutation that causes coiling and backward paralysis; locomotion in a loss of function mutant is nearly normal¹⁵. ds *unc-8* RNA or plasmid *hsp16-2_punc-8(IR)* was introduced into the n491 background and progeny were assayed for backing proficiency. Note that to regain backing ability, gene expression must be knocked down in the majority of *unc-8*-expressing cells, approximately 60 neurons.

C. elegans translation elongation factor 2 kinase eEF-2 (*efk-1*)¹¹ phosphorylates eEF-2, an activity abolished by a Tc1 insertion into the active site (A. Ryazanov, C. Mendola, L. Zhang and J. Culotti, unpublished observations) (Fig. 3a). We find that kinase activity in the offspring of heat-shocked *hsp16-2_pefk-1(IR)* transgenic parents is reduced at least several fold in 4/6 lines we assayed. An analogous assay could not be performed on a population of phenocopy mutants induced by conventional RNAi, since several hundred animals are required. We conclude that inducible IR genes are effective in generating populations amenable to biochemical analysis.

Injected dsRNA is not uniformly effective in

disrupting gene expression in the nervous system. For example, we find that only 6/210 progeny from three lines harboring integrated *unc-119_pGFP* (expressed in all neurons) injected with double-stranded GFP RNA exhibited a detectable reduction in fluorescence (Fig. 3b). To examine more closely effects of endogenously expressed dsRNA species on gene inactivation in the differentiated nervous system, we first constructed a plasmid that directs *in vivo* expression of double-stranded GFP RNA upon heat shock and tested for extinction of fluorescent signals generated by cell-specific GFP reporter fusions (Fig. 3b). We co-introduced the *hsp16-2_pGFP(IR)* construct and *unc-119_pGFP* (pIM175¹²; expressed at high levels throughout the nervous system¹³), selected lines exhibiting strong GFP fluorescence, heat shocked in the L4 stage, and examined fluorescence in their progeny. Approximately 79% of roller progeny from 3 (of 5) lines harboring *unc-119_pGFP* and *hsp16-2_pGFP(IR)* exhibit easily distinguished knockdown effects, with fewer than 10 cells readily detectable in most (Fig. 3b). We did not detect any consistent pattern of cells that appeared refractory to fluorescence inactivation, suggesting that all cells in the nervous system are susceptible to the effects of *in vivo* RNAi.

We also tested effects of heat shock induction of *hsp16-2_pGFP(IR)* on expression of an integrated *mec-4_pGFP* gene, which is specifically expressed in the six touch receptor neurons¹⁴. On average, 85% of roller progeny of heat shocked parents harboring the extragenic *hsp-16_pGFP(IR)* transgene had GFP signals that were either eliminated or markedly attenuated (2 of 4 lines; Fig. 3b). By contrast, we observed similar effects in only 11 of 270 progeny of a line harboring an integrated *mec-4_pGFP* reporter injected with dsGFP RNA.

We also tested for dsRNA-mediated inactivation of *C. elegans* neuronal genes. Conventional RNAi mediated by introduced *mec-4* dsRNA induced touch-insensitivity in 46/300 (15%) offspring of injected wild type parents.

5 On average, 60% progeny of heat-shocked lines harboring *hsp16-2_pmec-4(IR)* were touch insensitive (Table 1). As another example, we tested the effectiveness of *in vivo*-directed RNAi in the inactivation of *unc-8*, a neuronally expressed gene that in our hands has been resistant to

10 the effects of conventional RNAi. *unc-8* gain of function allele *n491* dominantly induces uncoordinated locomotion characterized by the inability to back up; the loss of function phenotype appears nearly wild type¹⁵. Injection of *unc-8* dsRNA is not effective in

15 knocking out the gf phenotype (2 phenocopy mutants generated among 1300 progeny of injected parents). Progeny of heat shocked *unc-8(n491)* mutants harboring *hsp16-2_punc-8(IR)* are effectively targeted about 13% of the time (Table 3). Taken together, our results

20 indicate that sequences expressed in terminally differentiated neurons can be targeted by *in vivo* induced RNAi and in some instances effects are more potent than those observed after injection of dsRNA.

For all nine cases we investigated, heat shock of

25 control lines carrying the expression vector alone or low temperature growth of lines carrying the *hsp16-2_p(IR)* genes did not produce any readily apparent phenotypes (we assayed for the anticipated knockout phenotype, morphological and locomotion defects, fertility, and

30 developmental abnormalities; >100 animals examined per line). Thus, effects of *in vivo* RNAi appear highly specific, consistent with reported tight regulation of the *hsp16-2* promoter⁸ and the selective precision of RNAi knock out capacity¹. Moreover, *in vivo* RNAi appears

effective in many tissue types, including neurons (Fig. 2b, note that *C37A2.5* and *efk-1* are expressed early in development and later in a broad range of cells including body wall and pharyngeal muscles, neurons, hypodermis and intestine (N. Tavernarakis, A. Ryazanov and M. Driscoll, unpublished); Mi2 homolog F2612.7 is expressed in the hypodermis; Mi2 homolog T14G8.1 is expressed in the hypodermis and pharynx (S. Wang, N. Tavernarakis and M. Driscoll unpublished); *myo-2* is expressed in pharyngeal tissue¹⁶).

Our analysis establishes that endogenous inverted repeat genes can be expressed to generate dsRNA species with biological effects similar to, and superior than that of directly injected dsRNA. Advantages of expressing heritable inverted repeat genes include that: 1) stable lines harboring the potential for gene inactivation can be easily maintained, 2) assays requiring large numbers of mutant phenocopies are feasible, and 3) inhibition can be inducible, and thus may be used for stage-specific gene inactivation. In some cases, the endogenous high level of dsRNA product produced upon heat shock appears to make for more potent inhibition than germline injected dsRNA. Although we have focused our initial studies on the use of the inducible *hsp16-2* promoter, our findings indicate that it is possible to inactivate specific genes for the duration of their expression period by integrating a transgene in which the promoter of the gene of interest drives transcription of an inverted repeat segment of the same gene. In addition, since dsRNA can inactivate genes in flies, plants, trypanosomes and planaria¹⁷⁻²⁰, *in vivo* directed RNAi could be effective in other organisms. These observations indicate that a similar strategy for *in vivo* driven RNAi can be applied to inactivate specific genes in organisms that can be

genetically engineered but are not readily amenable to direct injection of dsRNA.

5

Example II**IR CONSTRUCTS FOR USE IN THE PREVENTION AND TREATMENT OF
NEURODEGENERATIVE DISORDERS**

10 Neurodegenerative disorders, such as Alzheimer's and Parkinson's disease disproportionately affect the elderly, the most rapidly growing sector of the population. Additionally, many neural viral infections, such as those caused by HIV and encephalitis viruses, cause irreversible destruction of brain tissue, thereby
15 compromising the quality of life for the patient. Accordingly prophylactic and therapeutic treatments are highly desirable for preventing and/or inhibiting the neurodegeneration associated with such diseases.

20 Neurodegenerative disorders are generally classified as heritable or spontaneous in origin. Parkinson's disease (PD) and Alzheimer's disease (AD), appear to be both heritable and spontaneous diseases. Disorders such as spinocerebellar ataxia 1 and 3 are heritable diseases. Many of these disorders are
25 characterized by proteinaceous cellular inclusions (either inside or outside cells) encoded by genes whose expression is implicated in disease. In all cases, inappropriate accumulation of such proteinaceous cellular inclusions is associated with the progression
30 of the disease and, in some cases, is causally linked to disease etiology.

During viral infection and replication in brain tissue, harmful viral proteins accumulate and cellular destruction occurs. In HIV infection, CD4+ T cells are
35 targeted for destruction. During viral encephalitis,

neuronal cells are destroyed. Inhibition of viral replication can effectively prevent this type of neuronal cell damage.

5 Given that the aberrant, toxic accumulation of a cellular protein(s) to toxic levels is a theme common to diseases mentioned above and many other disorders, therapeutic treatments designed to reduce levels of such toxic proteins have general utility in the treatment of
10 patients suffering from neurodegenerative disorders. The present example provides compositions and methods suitable for reducing the levels of such toxic proteins utilizing RNAi generated from inheritable inverted repeat (IR) gene constructs. Such compositions can be
15 employed as a single agent or can be utilized in combination with other therapies. Such therapeutic approaches should result in an amelioration of symptoms associated with the disease and potentially reverse the course of the disease by eliminating the causative
20 agent. Moreover, the compositions and methods of the present invention may be used to advantage prophylactically to delay or prevent the onset of a disorder. This application has particular utility for preventing or delaying the onset of disease in patients
25 with a known genetic predisposition for a specific heritable neurodegenerative disorder.

 In the present example, the usefulness of the compositions and methods of the invention for the treatment of Alzheimer's disease (AD) and Parkinson's
30 disease is demonstrated.

 AD is a spontaneous neurodegenerative disorder which is caused by cell death in the brain and is characterized by the deposition of amyloid plaques. A major component of these plaques is β -amyloid, which is
35 a cleavage product of the amyloid precursor protein

(APP). Brain cell death is associated with an increase in a 42 amino acid fragment of β -amyloid, called A β , which is generated by an aberrant processing event of APP. A critical goal in AD therapy is the development of therapeutic agents which effectively reduce the production of this fragment.

To achieve this goal, an IR construct containing a fragment of DNA encoding A β can be placed under the control of a brain specific promoter. Following administration to a patient, which can be achieved by specific delivery to the brain or systemic introduction (see above), expression of the A β inverted repeat double stranded RNA molecule should dramatically reduce production of this neurotoxic A β fragment. This, in turn, should result in a dramatic reduction in plaque formation and delay or prevent disease onset.

An A β -IR expression construct can be generated as follows. A 1 kb fragment of A β nucleic acid is obtained. The GenBank Accession number for the genomic sequence of A β is D87675. The Genbank accession number for the cDNA is Y00264. The sequence can be amplified using A β specific primers that incorporate unique restriction sites at the IR fragment 5' and 3' ends and another restriction site to generate the inverted repeat which is ultimately situated at the inversion point (IP). See Figure 4. The 5' and 3' terminal restriction sites (designated as end A and B) can be used to insert the A β inverted repeat into an expression vector. Two A β products can then be generated in parallel by PCR amplification of human cDNA using (1) primers A and IP and (2) primers B and IP, respectively. Amplified A β fragments A-IP and B-IP can be digested with the appropriate restriction enzyme located at the IP restriction site (IPRS) to generate compatible termini which could then be ligated to produce an A β -IR.

Digestion of the A β -IR at the 5' and 3' restriction sites A and B facilitates ligation into an expression vector that has been linearized with restriction enzymes to generate compatible sites. The New England Biolabs catalog provides a wide variety of restriction enzymes and the corresponding restriction sites which can be utilized in the construction of the IR repeat constructs of the invention.

In an alternative cloning strategy, two naturally occurring restriction sites found within DNA encoding the A β fragment could be used to excise an A β fragment. In a two-step ligation reaction, this A β DNA fragment could be ligated end-to-end to generate an inverted repeat, and consequently ligated into an appropriately linearized vector as described above. In this cloning strategy it is necessary to treat the linearized expression vector with calf intestine alkaline phosphatase.

In yet another approach each of the desired sequence elements for the IR construct may be synthesized separately, blunt ended and then ligated using DNA ligase.

A variety of vectors are available for expressing exogenous nucleic acids in human cells. The plasmid vector pCEP4 (Invitrogen), for example, is comprised of components that facilitate selection and expression in human cells. pCEP4 contains the following elements: a CMV promoter, a TKpA - thymidine kinase polyadenylation signal, a Hygromycin resistance gene, a ColE1 origin, an Ampicillin resistance gene, an Epstein Barr Virus Nuclear Antigen (EBNA-1) and an EBV origin (OriP EBV) for episomal replication in EBV transformed cell. In another example, the plasmid clone pCR3 (Invitrogen) could also be used to drive high level IR gene expression in mammalian cells. This plasmid vector

includes a CMV promoter - Cytomegalovirus immediate-early promoter for high-level expression of the cloned IR gene; BGHpA - Bovine growth hormone polyadenylation signal for mRNA stability; ColE1 - origin for
5 replication, maintenance, and high copy number in *E. coli*; TKpA - thymidine kinase polyadenylation signal; Neomycin - neomycin resistance gene for selection of stable mammalian cell lines; PSV40/ori - origin for episomal replication in cells containing the SV40 large
10 T antigen; Ampicillin - resistance gene for selection and maintenance in *E. coli*; F1 ori-origin for rescue of sense strand for mutagenesis and single strand sequencing.

In another example, the CMV-Script-Ex vector
15 (Stratagene) could also be used to drive high level IR gene expression in mammalian cells. Several vectors suitable for use in the present invention are set forth in Table II.

Using Alzheimer's disease as an exemplary disease
20 model, and the β -amyloid encoding nucleic acid as the target for inhibition, the selected nucleic acid sequence corresponds to approximately 1000 contiguous nucleotides from the sequences set forth in the Genbank Accession Nos. provided above, operably linked in a
25 sense and antisense orientation. An exemplary expression construct for use in inhibiting the expression of beta-amyloid protein is shown in Figure 4.

As mentioned previously, the compositions and
30 methods of the invention also have utility in the treatment and prevention of Parkinson's disease. For example, alpha-synuclein has been implicated in the pathology of familial Parkinson's disease. The nucleic acid sequence encoding the alpha-synuclein protein is known. See Genbank Accession No. D31839. Accordingly,
35 an IR construct can be generated in accordance with the

present invention to reduce alpha synuclein accumulation in the affected patient. An appropriate expression vector for this purpose is shown in Figure 5, which contains 1081 nucleotides from GenBank Accession No. D31839 operably linked in a sense and antisense orientation. Methods for delivering the alpha-synuclein targeted IR constructs of the invention to the dopaminergic neurons of the substantia nigra (the neurons affected in the disease) are set forth hereinabove.

EXAMPLE III

USE OF IR GENE CONSTRUCT EXPRESSION VECTORS FOR CONTROLLING PLANT DISEASE

Geminiviruses are plant pathogens that infect a wide range of vegetable crops in tropical and subtropical regions with devastating consequences (Brown et al. (1992) Plant Disease, 76:220-225). Major epidemics of geminivirus infections of beans and tomatoes have occurred recently on several continents, thereby threatening the livelihood of farmers producing these crops and causing shortages which adversely impact the consumer population. The intransigent nature of the problem is underscored by a failure to generate cultivars that are resistant to geminiviruses by traditional breeding methods.

The compositions and methods of the invention are suitable for generating geminivirus resistant strains of a variety of vegetable crops that are susceptible to this family of viruses. In brief, the heritable system of RNAi described herein facilitates the generation of transgenic plant strains that produce dsRNA molecules which inhibit the expression of viral genes critical for productive infection. Transgenic plant strains can be engineered to express the inhibitory RNA molecule under

the control of either a constitutive or an inducible promoter. In one embodiment of the invention, an IR construct containing a fragment of DNA encoding an essential geminivirus protein may be placed under the control of a constitutive promoter that functions in plant cells. Viral genes encoding suitable target proteins for such inhibition include, but are not limited to, those essential for viral replication and capsid assembly. Plant cells transformed with such an IR gene construct expression vector should be resistant to viral infection. Progeny of plant cells containing stably integrated IR gene construct expression vectors inherit resistance to geminivirus infection. In a particularly preferred embodiment of the invention, the transformed plant cell is a seed from which resistant plant stock can be derived.

In the present example, an IR gene construct expression vector is described which can confer disease resistance to the tomato yellow leaf curl (TYLC) geminivirus. The TYLC virus infects the cultivated tomato (*Lycopersicon esculentum*), with devastating consequences. The virus which has a single monopartite genome, is a subgroup III type of geminivirus, transmitted by the whitefly. Navot, N. et al., (1991) Virology, 151-161. Notably, a whitefly-transmitted TYLC-like geminivirus having a bipartite genome has also been cloned. See Rochester, D. E., et al., (1990) Virology, 520-526.

The TYLC viral genome comprises six open reading frames. Two open reading frames, V1 and V2, are located on the virion or plus strand, whereas the four remaining open reading frames, C1, C2, C3, and C4 are located on the complementary or minus strand. The C2 open reading frame displays partial overlap with the C1 and C3 open reading frames. The C1 open reading frame,

which is sometimes referred to as AC1, includes the C4 open reading frame.

Partial or complete sequence data are available for several TYLC viral isolates. The entire genome of an Israeli isolate of TYLC virus, for example, has been cloned and sequenced. Navot, N. et al., (1991) Virology, 151-161. Sequence data are also available for TYLC viral isolates from Sardinia, Australia, Thailand, Egypt, and Sicily. Kheyr-Pour, A., et al., (1991) Nucl. Acids Res., 19:6763-6769. Dry et al. (1993) J Gen. Virol. 74:147-151. Padidam et al. (1995) J. Gen. Virol. 76:249-263. The entire genome sequence of the Tomato yellow leaf curl virus can be found at GenBank Accession No. NC_001996.

In an exemplary IR gene construct expression vector, the geminivirus Nia-protease (NP) gene, which is required for productive infection is targeted for gene silencing. A fragment of DNA which encodes a portion of the NP can be generated from either PCR of available TYLC isolates or by RT-PCR of RNA derived from infected plant cells amplified using suitable forward and reverse primers. Suitable primer sequences corresponding to NP (of approximately 20-25 bases) can be selected from sequence information available in a variety of data bases. The NP specific primers are designed to incorporate unique restriction sites at the IR fragment 5' and 3' ends and another unique restriction site to generate the inverted repeat which is ultimately situated at the inversion point (IP) (See figure). The 5' and 3' terminal restriction sites (designated as end A and B) can be used to insert the NP inverted repeat into a plant expression vector of choice. Specifically, two NP products would be generated in parallel by PCR amplification of TYLC genomic DNA or cDNA using (1) primers A and IP and (2) primers B and IP,

respectively. Amplified NP fragments A-IP and B-IP would be digested with the appropriate restriction enzyme located at the IP restriction site (IPRS) to generate compatible termini which could then be ligated to produce an NP-IR. Digestion of the NP-IR at the 5' and 3' restriction sites A and B facilitates ligation into a plant expression vector that has been linearized with restriction enzymes to generate compatible sites.

In an alternative cloning strategy, two naturally occurring restriction sites found within an NP gene fragment could be used to excise the fragment. In a two-step ligation reaction, this NP fragment could be ligated end-to-end to generate an inverted repeat, and consequently ligated into an appropriately linearized expression vector as described above. In this cloning strategy it is suggested to treat the linearized expression vector with calf intestine alkaline phosphatase to prevent the recircularization of vector without the incorporation of the desired NP-IR insert.

In yet another approach, each of the IR gene construct expression vector sequence elements may be cloned and isolated separately and then operably linked into an expression vector using DNA ligase. As mentioned previously, the first and second coding regions of the IR gene construct may optionally include a spacer sequence between the first and second coding sequences to facilitate expression or stability of the clone.

A variety of plant expression vectors are available that would be of utility for the present invention. In a preferred embodiment of the invention, the cauliflower mosaic virus derived expression vector CMV35S could be utilized to drive expression of the NP-IR in tomato cells (Gleave, 1992).

Once fully constructed, the NP-IR expression vector

would then be transformed into a suitable bacterial strain such as, for example, *E. coli* strain DH5 or SURE. Transformation into bacteria facilitates the generation of large quantities NP-IR expression vector, which can
5 be used in the production of TYLC resistant tomato plant strains.

In one application of the present invention, tomato plants are transformed using *Agrobacterium* which requires a T-DNA producing binary vector (pBIN19 for
10 example, Stanford et al., 1990). In another application of the present invention, tomato plants can be transformed using particle bombardment, for which there are no requirements for specific DNA constructs.

Methods are available for the isolation of stable
15 plant transformants. In a preferred embodiment, the IR gene construct expression vector optionally includes a selectable marker gene. Such markers include, but are not limited to, the NPTII gene which confers resistance to the antibiotic kanamycin or the BAR gene which
20 confers resistance to the plant herbicide Bialophos. Examples of tobacco vectors are: pART7 and pART 27 (Gleave, 1992 Plant Mol. Biol. 20: 1203-1207). A suitable rice vector is pVec4 (Wang et al., 1998 Acta Hortic. 461:401-405.).

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5

While certain preferred embodiments of the present invention have been described and specifically exemplified above, it is not intended that the invention be limited to such embodiments. Various modifications
10 may be made to the invention without departing from the scope and spirit thereof as set forth in the following claims.

What is claimed is:

1. An IR gene construct encoding an inverted repeat gene, said construct comprising:

5 a) a promoter element operably linked in a 5' to 3' direction to a first coding sequence and a second sequence, said first coding sequence being in a sense orientation, said second sequence being the first coding sequence in an antisense orientation; and

10 b) a transcription termination element operably linked 3' to said first and second coding sequences.

15 2. The IR gene construct of claim 1 inserted into an expression vector.

 3. A IR gene construct as claimed in claim 1, said promoter being inducible.

20 4. A IR gene construct as claimed in claim 2, said promoter being selected from the group consisting of a heat shock promoter, a metallothioneine promoter, a glucocorticoid promoter, CMV promoter, SV40 promoter, nervous system specific promoters, unc-119, mec-4, odr-4, muscle promoters unc-54, myo-2, act-1 and ben-1, and a CaMV promoter.

30 5. The DNA construct of claim 1, wherein a spacer sequence is inserted between said first coding and second sequences.

 6. A host cell containing the DNA construct of claim 1.

35 7. A method for production of a phenocopy

knock out mutant by introducing an inverted repeat gene into an organism, said inverted repeat gene comprising:

a) a promoter element operably linked in a 5' to 3' direction to a first coding sequence and a second sequence, said first coding sequence being in a sense orientation, said second sequence being the first coding sequence in an antisense orientation; and

b) a transcription termination element operably linked 3' to said first and second coding sequences.

8. A method as claimed in claim 7, wherein said inverted repeat gene is introduced into *C. elegans* via a process selected from the group consisting of microinjection, soaking, and DNA coated particle bombardment.

9. A method as claimed in claim 7, wherein said inverted repeat gene contains the coding sequence of a gene selected from the group consisting of green fluorescent protein gene, C3782.5, F26F12.7, T14G8.1, *efk-1*, *mec-4*, *unc-8*, *unc-119*, *degenerinis* ZB770.1, T28B8.5, T28F24.2, C24G7.2 and T28D9.7.

10. A method as claimed in claim 7, wherein said inverted repeat gene is passed onto progeny thereby generating phenocopy mutants upon induction of expression of said inverted repeat gene.

11. A method as claimed in claim 7, wherein said organism is selected from the group consisting of plants, mice, humans, insects and nematodes.

12. An IR gene construct expression vector as claimed in claim 2 for the treatment of Alzheimers

disease as shown in Figure 4.

13. An IR gene construct expression vector as
claimed in claim 2 for the treatment of Parkinson's
5 disease as shown in Figure 5.

14. An IR gene construct expression vector as
claimed in claim 2 for the treatment of tomato leaf curl
geminivirus as shown in Figure 6.
10

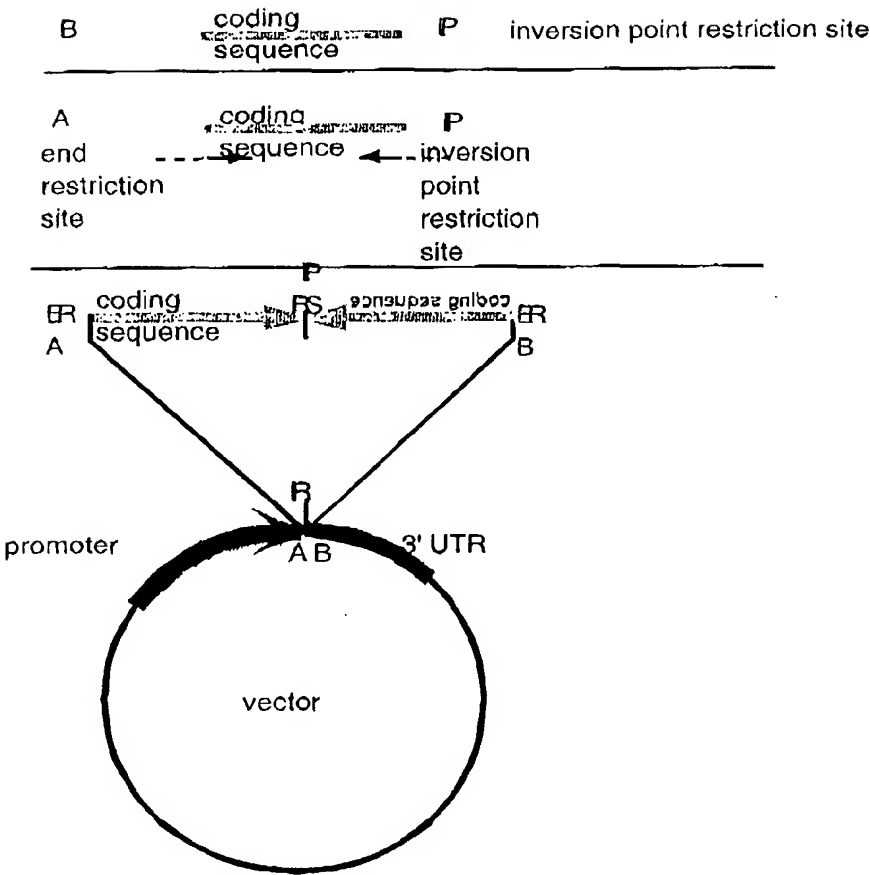
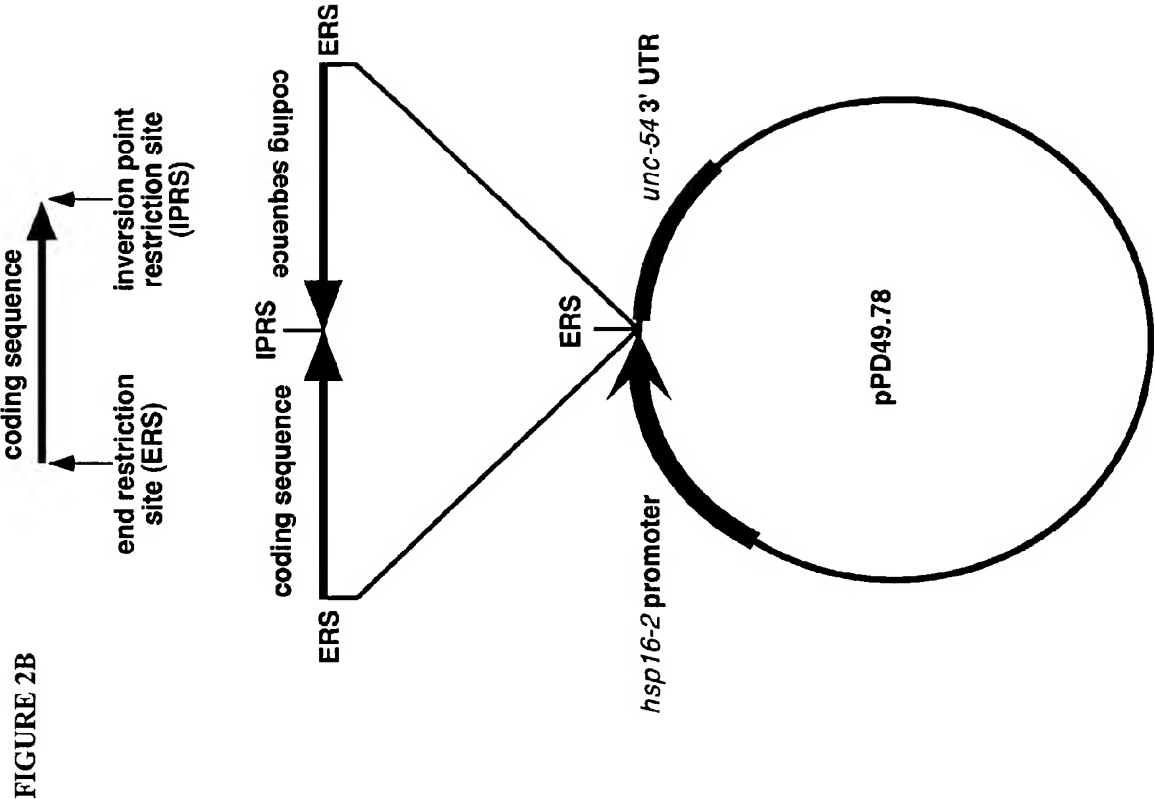


FIGURE 1



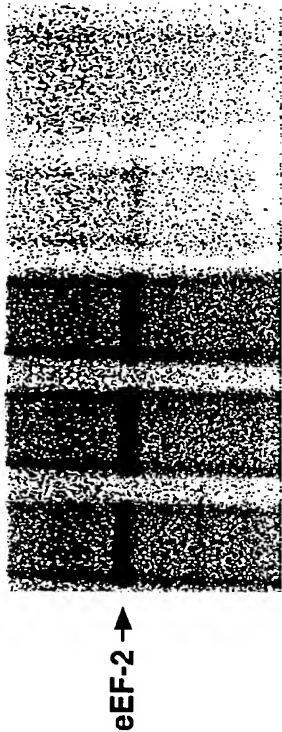
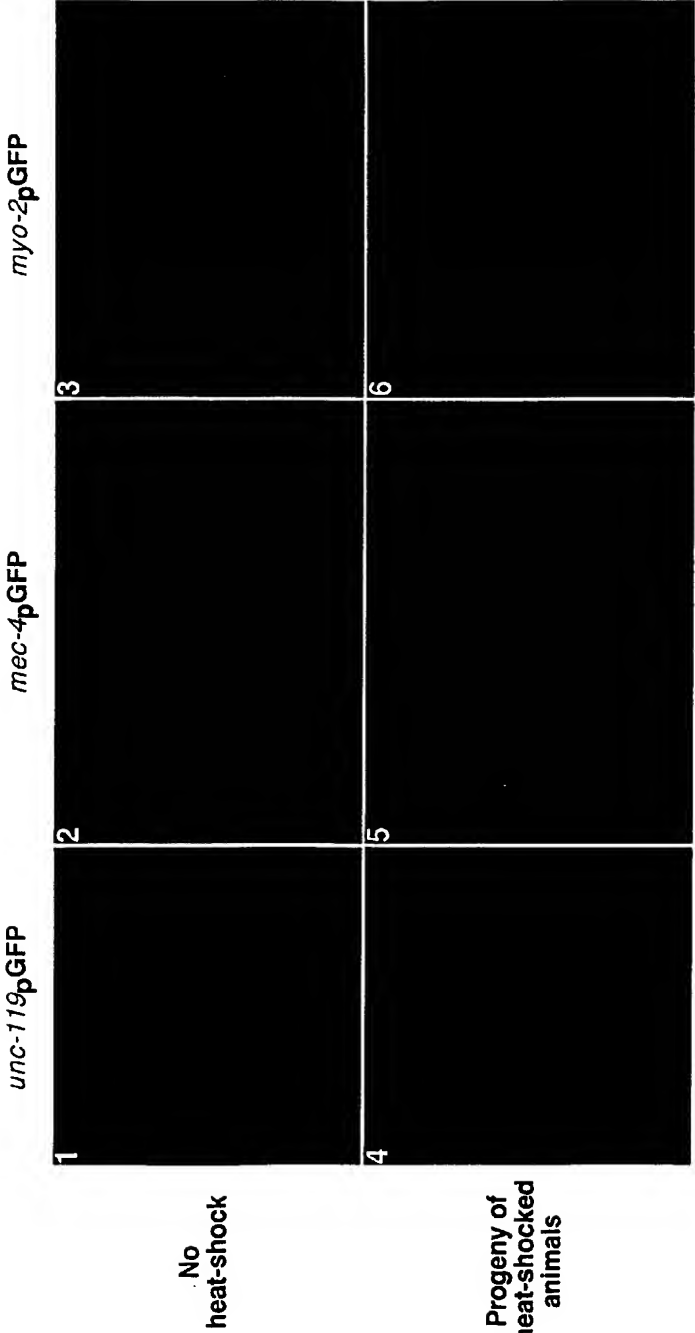


FIGURE 3A

FIGURE 3B



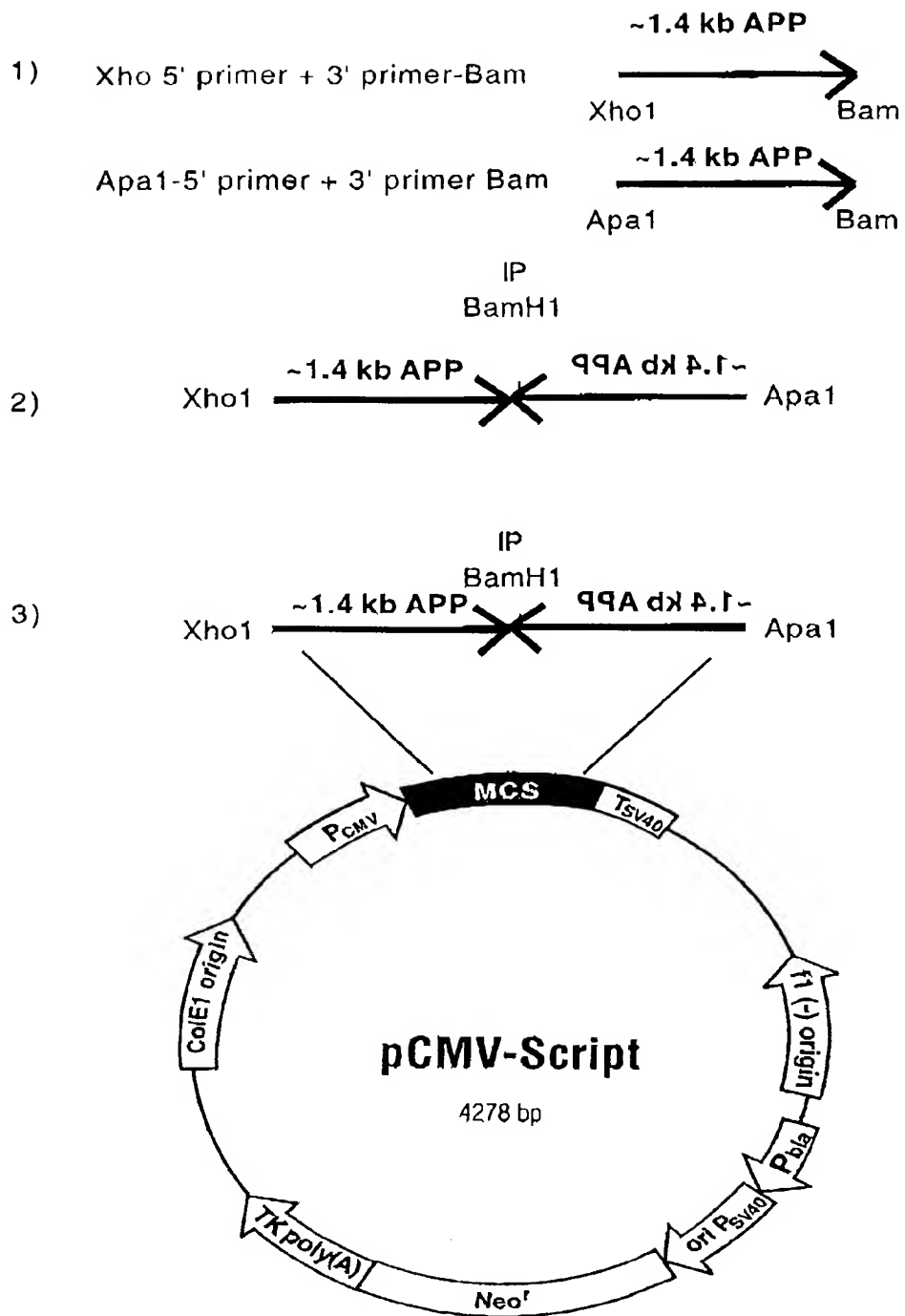


FIGURE 4

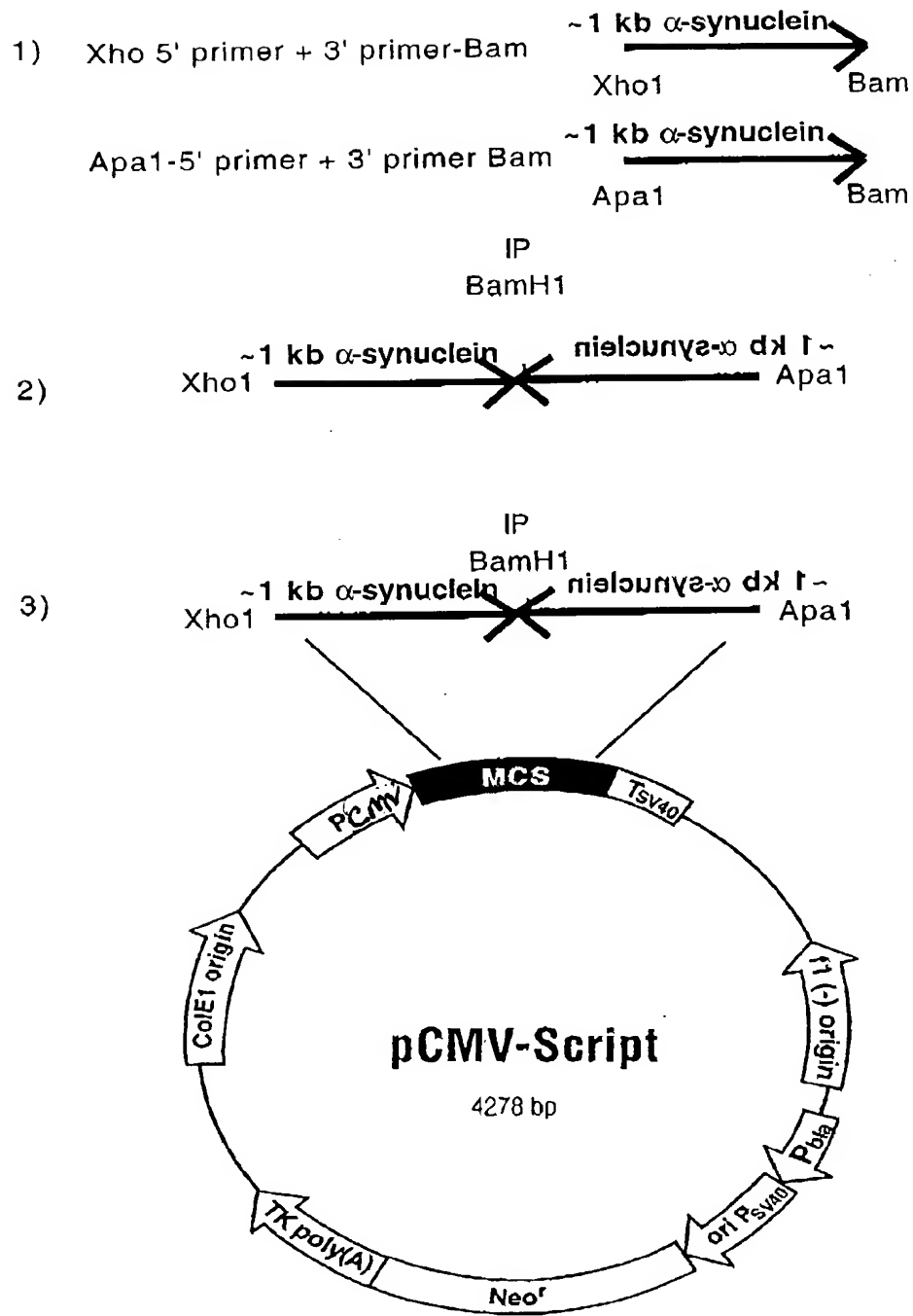


FIGURE 5

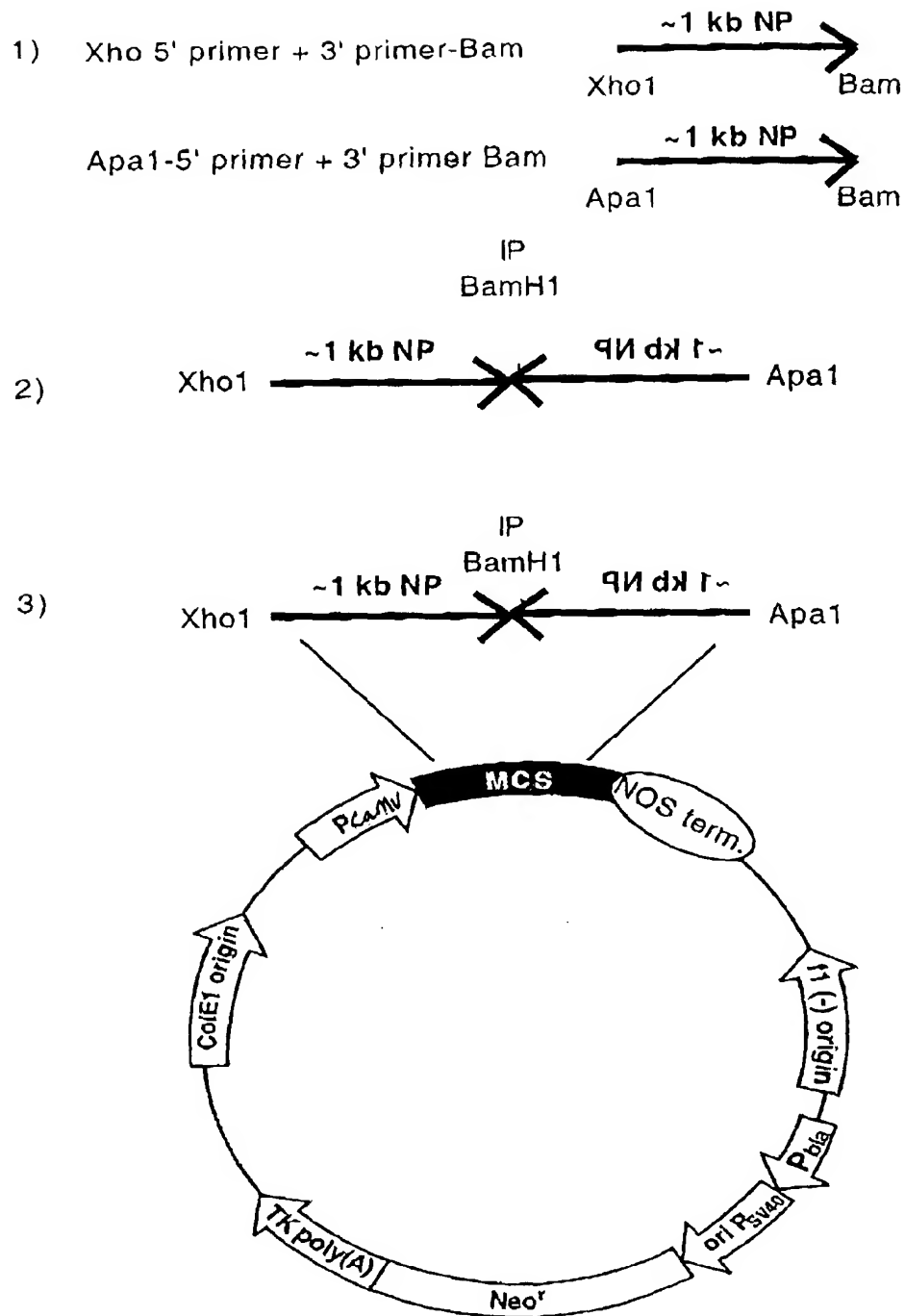


FIGURE 6